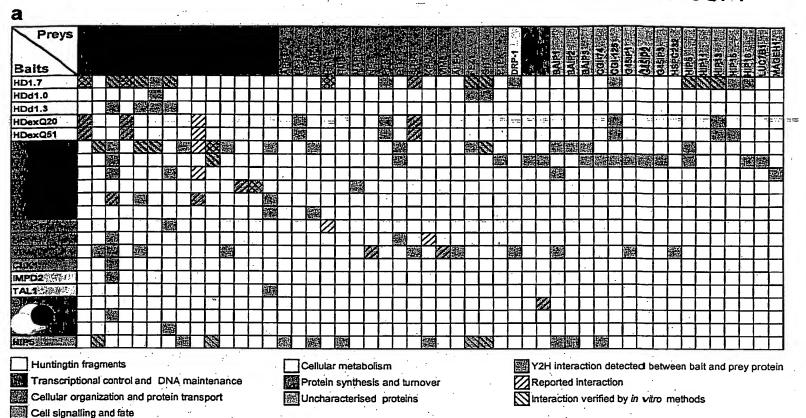


Figure 1



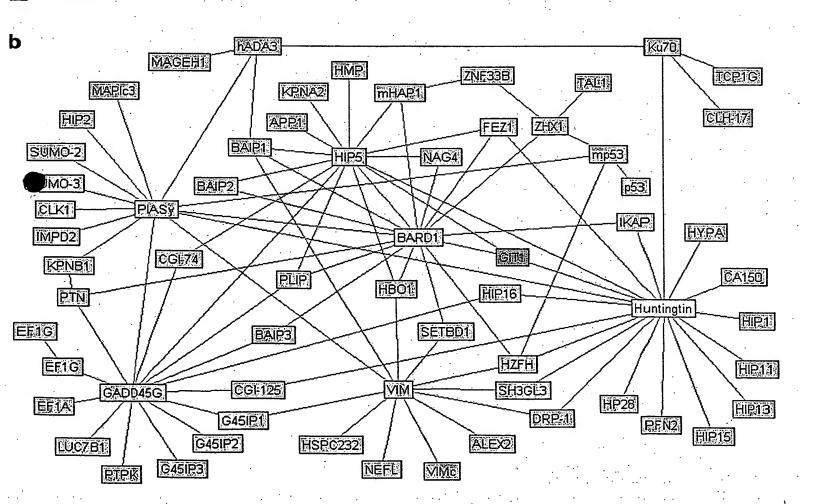
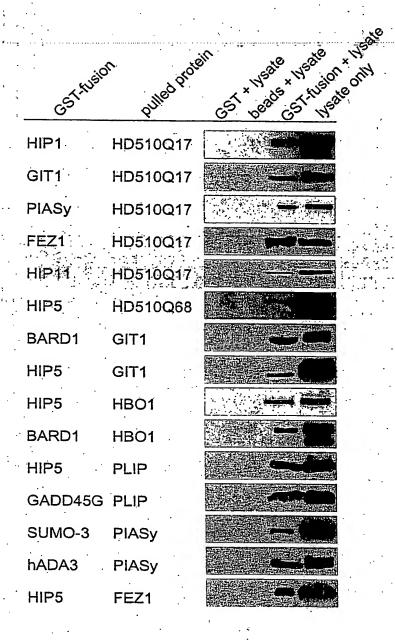
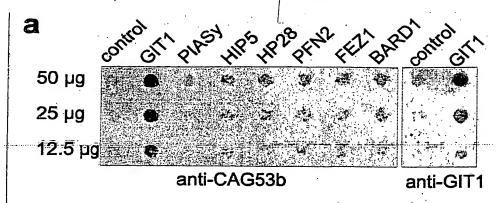
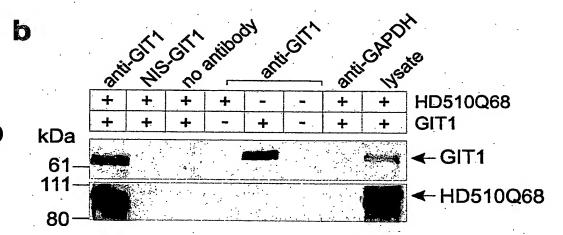


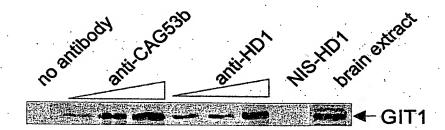
Figure 2

# BEST AVAILABLE COPY









C



HD510Q68 + GIT1

Figure 4

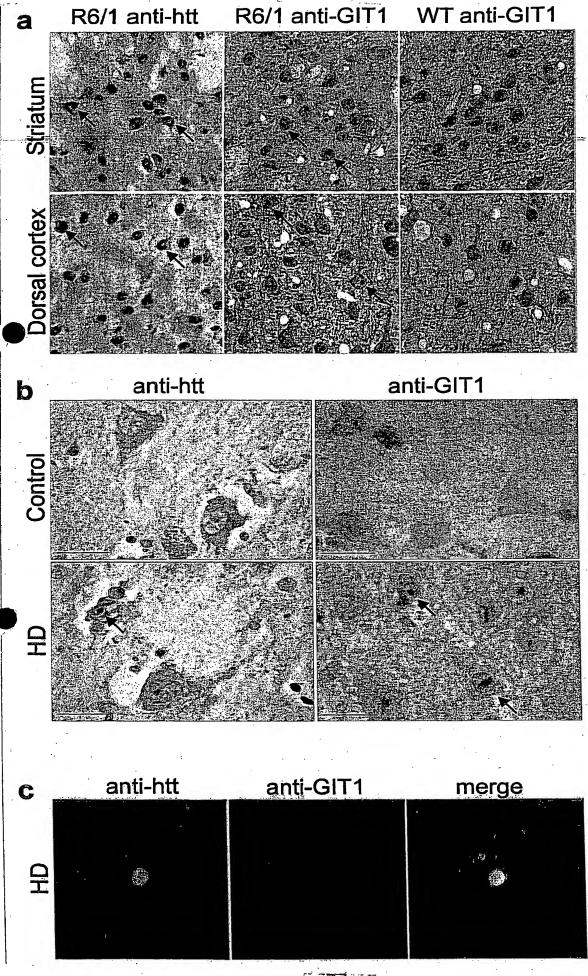


Figure 5

#### >ALEX2

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ATPGAHTGAIPKATSATGAVPKGGGKGVTRSRNGGKGKGKKSKVEVDELGMGFRPGDGAAAJAAAS
ANGGQAFLAEVPDSEEGESGWTDTESDSDSEPETQRRGRGRRPVAMQKRPFPYEIDEILGVRDLRK
VLALLQKSDDPFIQQVALLTLSNNANYSCNQETIRKLGGLPIIANMINKTDPHIKEKALMAMNNLS
ENYENQGRLQVYMNKVMDDIMASNINSAVQVVGLKFLTNMTITNDYQHLLVNSIANFFRLLSQGGG
KIKVEILKILSNFAENPDMLKKLLSTQVPASFSSLYNSYVESBILINALTLFEIIYDNLRAEVFNY
REFNKGSLFYLCTTSGVCVKKIRALANHHDLLVKVKVIKLVNKF

EEEEESFPQPVDDYFVEPPQAEEEEETVPPPSSHTLAVVGKVTPTPRPTDGVDIYFGMPGEISEHE GFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADRQALNEHFQSILQTLEEQVSGERQRLVE THATRVIALINDQRRAALEGFLAALQADPPQAERVLLALRRYLRAEQKEQRHTLRHYQHVAAVDPE KAQQMRFQVHTHLQVIEERVNQSLGLLDQNPHLAQELRPQIQELLHSEHLGPSELEAPAPGGSSED KGGLQPPDSKDDTPMTLPKGSTEQDAASPEKEKMNPLEQYERKVNASVPGVSLSTHRRFRGMSWHQLGQGCPVRLCRVC

## >BAIP1

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#### >BAIP2

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## >BAIP3

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## >BARD1

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QQFIPGPLKILVWPCCLFSQAPTTQDQTPSSAVSVATPTVSVSTPAPTATPVQTVPQPHPQTLPPA VPHSVPQPTTAIPAFPPVMVPPFRVPLPGMPIPLPGVLPGMAPPIVPMIHPQVAIAASPATLAGAT AVSEWTEYKTADGKTYYYNNRTLESTWEKPQELKEKEKLEEKIKEPIKEPSEEPLPMETEEEDPKE EPIKEIKEEPKEEEMTEEEKAAQKAKPVATAPIPGTPWCVVWTGDERVFFYNPTTRLSMWDRPDDL IGRADVDKIIQEPPHKKGMEELKKLRHPTPTMLSIQKWQFSMSAIKEEQELMEEINEDEPVKAKKR

K

>CGI-125

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>CGI-74

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>CLH-17

MAQILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPI SADSAIMNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSM EGESQPVKMFDRHSSLAGCQIINYRTDAKQKWLLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHA ASFAQFKMEGNAEESTLFCFAVRGQAGGKLHIIEVGTPPTGNQPFPKKAVDVFFPPEAQNDFPVAM QISEKHDVVFLITKYGYIHLYDLET

>CLK1

DAWVLEHLNTTDPNSTFRCVQMLEWFEHHGHICIVFELLGLSTYDFIKENGFLPFRLDHIRKMAYQ ICKSVNFLHSNKLTHTDLKPENILFVQSDYTEAYNPKIKRDERTLINPDIKVVDFGSATYDDEHHS TLVSTKHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFPTHDSKEHLAMMERILGPLPKHMI QKTRKRKYFHHDRLDWDEHSSAGRYVSRRCKPLKEFMLSQDVEHERLFDLIQKMLEYDPAKRITLR EALKHPFFDLLKKSI

>DRP-1

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>EF1A

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>EF1G(bait)

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>EF1G (prey)

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>G45IP3

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>hADA3

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>HD1.7

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>HDexQ20

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>HDexQ51

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>HIP11

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>HIP13

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DEEERNHRQMIKEAFAGDDVIRDFLKEKREAVEASKPKDVDLTLPGWGEWGGVGLKPSAKKRRRFL IKAPEGPPRKDKNLPNVIINEKRNIHAAAHQVRVLPYPFTHHWQFERTIQTPIGSTWNTQRAFQKL TTPKVVTKPGHIINPIKAEDVGYRSSSRSDLSVIQRNPKRITTRHKKQLKKCSVD >HIP2

MANIAVQRIKREFKEVLKSEETSKNQIKVDLVDENFTELRGEIAGPPDTPYEGGRYQLEIKIPETY PFNPPKVRFITKIWHPNISSVTGAICLDTLKDQWAAAMTLRTVLLSLQAILAAAEPDDPQDAVVAN QYKQNPEMFKQTARLWAHVYAGAPVSSPEYTKKIENLCAMGFDRNAVIVALSSKSWDVETATELLL SNX

>HIP5 (bait)

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>HIP5 (prey)

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>HMP

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>HP28

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### >HYPA

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>HZFH

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>IKAP

LKEGSPLEDLALLEALSEVVQNTENLKDEVYHILKVLFLFEFDEQGRELQKAFEDTLQLMERSLPE IWTLTYQQNSATPVLGPNSTANSIMASYQQQKTSVPVLDAELFIPPKINRRTQWKLSLLD >IMPD2

DFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEF QANEVRKVKKYEQGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDF LKEEEHDCFLEEIMTKREDLVVAPAGITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNR DYPLASKDAKKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNL QVIGGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVPVIA DGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNR YFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVRAMMYSGELKFEKRTS SAQVEGGVHSLHSYEKRLF

>KPNA2

AWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGDGSVFRDLVIKYGAV
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TSGGTVEQIVYLVHCGIIEPLMNLLTAKDTKIILVILDAISNIFQAAEKLGETEKLSIMIEECGGL
DKIEALQNHENESVYKASLSLIEKYFSVEEEEDQNVVPETTSEGYTFQVQDGAPGTFNF
>KPNB1

LAAVGLVGDLCRALQSNIIPFCDEVMQLLLENLGNENVHRSVKPQILSVFGDIALAIGGEFKKYLE VVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQENVHPDVMLVQPRVEFILS FIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLATWA TKELRKLKNQA

>Ku70

KTRTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHYLRP SLFVYPEESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQKIQVTPP GFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRSDSFENPVLQQHFRNLEALALD LMEPEQAVDLTLPKVEAMNKRLGSLVDEFKELVYPPDYNPEGKVTKRKHDNEGSGSKRPKVEYSEE ELKTHISKGTLGKFTVPMLKEACRAYGLKSGLKKQELLEALTKHFQD >LUC781

VDAVAVDAAAVSAKAEKVHELNEKIGKLLAKAEQLGAEGNVDESQKILMEVEKVRAKKKEAEEEYR NSMPASSFQQQKLRVCEVCSAYLGLHDNDRRLADHFGGKLHLGFIQIREKLDQLRKTVAEKQEKRN QDRLRREEREREERLSRRSGSRTRDRRRSRSRDRRRRSRSTSRERRKLSRSRSRDRHRRHRSRS RSHSRGHRRASRDRSAKYKFSRERASREESWESGRSERGPPDWRLESSNGKMASRRSEEKEAGEI >MAGEH1

ASFPRTAVSFEPLAGDMPRGRKSRRRRNARAAEENRNNRKIQASEASETPMAASVVASTPEDDLSG PEEDPSTPEEASTTPEEASSTAQAQKPSVPRSNFQGTKKSLLMSILALIFIMGNSAKEALVWKVLG KLGMQPGRQHSIFGDPKKIVTEEFVRRGYLIYKPVPRSSPVEYEFFWGPRAHVESSKLKVMHFVAR VRNRCSKDWPCNYDWDSDDDAEVEAILNSGARGYSAP >MAP11c3

QRRSFADRCKEVQQIRDQHPSKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELVKIIRRRLQLN PTQAFFLLVNQHSMVSVSTPIADIYEQEKDEDGFLYMVYASQETFGF >mHAP1

PKEQVQSGAGDGTGSGDPAAGTPTTQPAVGPAPEPSAEPKPAPAQGTGSGQKSGSRTKTGSFCRSM IIGDSDAPWTRYVFQGPYGPRATGLGTGKAEGIWKTPAAYIGRRPGVSGPERAAFIRELQEALCPN PPPTKKITEDDVKVMLYLLEEKERDLNTAARIGQSLVKQNSVLMEENNKLETMLGSAREEILHLRK QVNLRDDLLQLYSDSDDDDDEEDEEDEEEGEEEREGQRDQDQQHDHPYGAPKPHPKAETAHRCPQ LETLQQKLRLLEEENDHLREEASHLDNLEDEEQMLILECVEQFSEASQQMAELSEVLVLRLEGYER QQKEITQLQAEITKLQQRCQSYGAQTEKLQQMLASEKGIHSESLRAGSYMQDYGSRPRDRQEDGKS HRQRSSMPAGSVTHYGYSVPLDALPSFPETLAEELRTSLRKFITDPAYFMERRDTHCREGRKKEQR AMPPPPAX

>mp53

VTETPGPVAPAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTC PVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLE DRQTFRHSVVVPYEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVR VCACPGRDRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKRFE MFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD

RDRVENEAEKDLQCHAPVRLDLPPEKPLTSSLAKQEEVEQTPLQEALNQLMRQLQRKDPSAFFSFP
VTDFIAPGYSMIIKHPMDFSTMKEKIKNNDYQSIEELKDNFKLMCTNAMIYNKPETIYYKAAKKLL
HSGMKILSQERIQSLKQSIDFMADLQKTRKQKDGTDTSQSGEDGGCWQREREDSGDAEAHAFKSPS
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TRTLDTAKEMEITEVEPPGRLDSSTQDRLIALKAVTNFGVPVEVFDSEEAEIFQKKLDETTRLLRE
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MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGPDEAPRM PEAAPPVAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNK MFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVE GNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGEPHHELPPGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD

.....

>PFN2

APRRPRCSAKGSKMAGWQSYVDNLMCDGCCQEAAIVGYCDAKYVWAATAGGVFQSITPIEIDMIVG  ${\tt KDREGFFINGLTLGAKKCSVIRDSLYVDGDCTMDIRTKSQGGEPTYNVAVGRAGRVLVFVMGKEGV}$ HGGGLNKKAYSMAKYLRDSGF

>PIASy(bait)

LVEAKNMYMSFRVSDLOMLLGFVGRSKSGLKHELVTRALQLVQFDCSPELFKKTKELYETRYAKKN SEPAPOPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRLPAKTLKPEVRLVKL PFFNMLDELLKPTELVPQNNEKLQESPCIFALTPRQVELIRNSRELQPGVKAVQVVLRICYSDTSC PQEDQYPPNIAVKVNHSYCSVPGYYPSNKPGVEPKRPCRPINLTHLMYLSSATNRITVTWGNYGKS YSVALYLVRQLTSSELLQRLKTIGVKHPELCKALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLS VPCRAETCAHLQCFDAVFYLQMNEKKPTWMCPVCDKPAPYDQLIIDGLLSKILSECEDADEIEYLV DG\$WCPIRAEKERSC\$PQGAILVLGPSDANGLLPAP\$VNG\$GALG\$TGGGGPVG\$MENGKPGADVV DLTLDSSSSSEDEEEEEEEEEDEDEEGPRPKRRCPFQKGLVPAC

>PIASy (prey)

LVEAKNMVMSFRVSDLQMLLGFVGRSKSGLKHELVTRALQLVQFDCSPELFKKIKELYBTRYAKKN SEPAPQPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRLPAKTLKPEVRLVKL PFFNMLDELLKPTELVPQNNEKLQESPCIFALTPRQVELIRNSRELQPGVKAVQVVLRICYSDTSC PQEDQYPPNIAVKVNHSYCSVPGYYPSNKPGVEPKRPCRPINLTHLMYLSSATNRITVTWGNYGKS YSVALYLVRQLTSSELLQRLKTIGVKHPELCKALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLS VPCRAETCAHLQCFDAVFYLQMNEKKPTWMCPVCDKPAPYDQLIIDGLLSKILSECEDADEIEYLV DGSWCPIRAEKERSCSPQGAILVLGPSDANGLLPAPSVNGSGALGSTGGGGPVGSMENGKPGADVV DLTLDSSSSSEDEEEEEEEEEDEDEEGPRPKRRCPFQKGLVPAC . >PLIP

GEIIEGCRLPVLRRNQDNEDEWPLAEILSVKDISGRKLFYVHYIDFNKRLDEWVTHERLDLKKIQF PKKEAKTPTKNGLPGSRPGSPEREVKRKVEVVSPATPVPSETAPASVFPQNGAARRAVAAQPGRKR KSNCLGTDEDSQDSSDGIPSAPRMTGSLVSDRSHDDIVTRMKNIECIELGRHRLKPWYFSPYPQEL TTLPVLYLCEFCLKYGRSLKCLQRHLTKCDLRHPPGNEIYRKGTISFFEIDGRKNKSYSQNLCLLA KCFLDHKTLYYDTDPFLFYVMTEYDCKGFHIVGYFSKEKESTEDYNVACILTLPPYQRRGYGKLLI EFSYELSKVEGKTGTPEKPLSDLGLLSYRSYWSQTILEILMGLKSESGERPQITINEISEITSIKK EDVISTLQYLNLINYYKGQYILTLSEDIVDGHERAMLKRLLRIDSKCLHFTPKDWSKRGKW >PTN

LSQRQDQVPRLPVQKSRQESPRAEENPKWREGKKETSESSVQKAGRAAAQAGAAASRVPGLSGSN LAPCNKGRLSAREDVSNSKMQAQQYQQQRRKFAAAFLAFIFILAAVDTAEAGKKEKPEKKVKKSDC GEWQWSVCVPTSGDCGLGTREGTRTGAECKQTMKTQRCKIPCNWKKQFGAECKYQFQAWGECDLNT ALKTRTGSLKRALHNAECQKTVTISKPCGKLTKPKPQAESKKKKKEGKKQEKMLD >PTPK

SNYINAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEVDLSQGCPQYWPEEGML RYGPIQVECMSCSMDCDVINRIFRICNLTRPQEGYLMVQQFQYLGWASHREVPGSKRSFLKLILQV EKWQEECEEGEGRTIIHCLNGGGRSGMFCAIGIVVEMVKRQNVVDVFHAVKTLRNSKPNMVEAPEQ YRFCYDVALEYLESS

>SETBD1

 $\tt KASTSGLGIKDEGDIKQAKKEDTDDRNKMSVVTESSRNYGYNPSPVKPEGLRRPPSKTSMHQSRRL$  ${\tt MASAQSNPDDVLTLSSSTESEGESGTSRKPTAGQTSATAVDSDDIQTISSGSEGDDFEDKKNMTGP}$ MKRQVAVKSTRGFALKSTHGIAIKSTNMASVDKGESAPVRKNTRQFYDGEESCYIIDAKLEGNLGR YLNHSCSPNLFVQNVFVDTHDLRFPWVAFFASKRIRAGTELTWDYNYEVGSVEGKELLCCCGAIEC RGRLL .

.>SH3GL3

VAGLKKOFHKASQLFSEKISGAEGTKLDDEFLDMERKIDVTNKVVAEILSKTTEYLQPNPAYRAKL GMLNTVSKIRGQVKTTGYPQTEGLLGDCMLKYGKELGEDSTFGNALIEVGESMKLMAEVKDSLDIN VKÖTFIDPLQLLQDKDLKEIGHHLKKLEGRRLDYDYKKKRVGKIPDEEVRQAVEKFEESKELAERS MFNFLENDVEQVSQLAVFIEAALDYHRQSTEILQELQSKLQMRISAASSVPRREYKPRPVKRSSSE LNGVSTTSVVKTTGSNIPMDQPCCRGLYDFEPFNQGELGFKEGDITTLTNQTDENWYEGMTHGESG FFPINYVEVIVPLPQ

>SUMO-2

RPRAQLERESGAESVTRPLRAASPAPPPRAARAAMSEEKPKEGVKTENDHINLKVAGQDGSVVQF KIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPAQLEMEDEDTIDVFQQQTGGVPESS LAGHSF

>SUMO-3

PSSTAAASFFCRSWCCLCARLVRTWYLFCEAAAEETPALAMADEKPKEGVKTENNDHINLKVAGOD GSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPAQLEMEDEDTIDVFQQQTG GVY

>TAL1

SSPVKRQRMESALDQLKQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAY GRKLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKEAGI SKDRILIKLSSTWEGIQAGKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFVGRILDWHVAN TDKKSYEPLEDPGVKSVTKIYNYYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISPKLLGELLQD NAKLVPVLSAKAAQASDLEKIHLDEKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN AENGK

>TCPG

QTDIEITREEDFTRILQMEEEYIQQLCEDIIQLKPDVVITEKGISDLAQHYLMRANITAIRRVRKT DNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDCKDPKACTILLRGASKEIL SEVERNLQDAMQVCRNVLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRT LIQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLL LRIDDIVSGHKKKGDDQSRQGGAPDAGQE

>VIM

SPRQRRSRAPTTHTHRALVRLFSGSQSAPPPPPRPSPPSAAMSTRSVSSSSYRRMFGGPGTASRPS SSRSYVTTSTRTYSLGSALRPSTSRSLYASSPGGVYATRSSAVRLRSSVPGVRLLQDSVDFSLÄDA INTEFKNTRTNEKVELQELNDRFÄNYIDKVRFLEQQNKILLAELEQLKGQGKSRLGDLYEEEMREL RRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFRODVDNASLARLDLERK VESLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVAAKNIQEAEE WYKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEENFAVEA ANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLLEGEESRISLPLPNFSSL NLRETNLDSLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE >VIMC

QEEMLOREEAENTLOSFRODVDNASLARLDLERKVESLOEEIAFLKKLHEEEIOELOAQIQEOHVO IDVDVSKPDLTAALRDVRQQYESVAAKNLOEAEEWYKSKFADLSEAANRNNDALROAKQESTEYRR QVQSLTCEVDALKGTNESLEROMREMEENFÄVEAANYQDTIGRLODEIONMKEEMARHLREYODLL NVKMALDIEIATYRKLLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTLLIKTVETRDGQ VINETSOHHDDLE

## >ZHX1

EQTINDLTFDGSFVKEENAEQAESTEVSSGISISKTPIMKMMKNKVENKRIAVHHNSVEDVPEEK ENEIKPDREEIVENPSSSASESNTSTSIVNRIHPSTASTVVTPAAVLPGLAQVITAVSAQQNSNLI PKVLIPVNSIPTYNAALDNNPLLLNTYNKFPYPTMSEITVLSAQAKYTEEQIKIWFSAQRLKHGVS WTPEEVEEARRKQFNGTVHTVPQTITVIPTHISTGSNGLPSILQTCQIVGQPGLVLTQVAGTNTLP VTAPIALTVAGVPSQNNIQKSQVPAAQPTAETKPATAAVPTSQSVKHETALVNPDSFGIRAKKTKE QLAELKVSYLKNQFPHDSEIIRLMKITGLTKGEIKKWFSDTRYNQRNSKSNQCLHLNNDSSTTIII DSSDETTESPTVGTAQPKQSWNPFPDFTPQKFKEKTAEQLRVLQASFLNSSVLTDEELNRLRAQTK LTRREIDAWFTEKKKSKALKEEKMEIDESNAGSSKEEAGETSPADESGAPKSGSTGKICKKTPEQL HMLKSAFVRTQWPSPEEYDKLAKESGLARTDIVSWFGDTRYAWKNGNLKWYYYYQSANSSSMNGLS SLRKRGRGRPKGRGRPRGRPRGSKRINNWDRGPSLIKFKTGTAILKDYYLKHKFLNEQDLDELV NKSHMGYEQVREWFAERQRRSELGIELFEENEEEDEVIDDQEEDEEETDDSDTWEPPRHVKRKLSK SDD

#### >ZNF33B

CYECGKTFCLKSDLTIHQRTHTGEKPFACPECGKFFSHKSTLSQHYRTHTGEKPYECHECGKIFYN KSYLTKHNRTHTGEKPYECNECGKTFCQKSQLTQHQRIHIGEKPYECNECGKAFCHKSALIVHQRT HTQEKPYKCNECGKSFCVKSGLILHERKHTGEKPYECNECGKSFSHKSSLTVHYRAHTGEKSCQCN ECGKIFYRKSDLAKHQRSHTGEKPYECNTCRKTFSQKSNLIVHQRTHIGEKPYE

#### >ALEX2

GCCGAATCAGTAGTTGGGGCTGCAATGGCTTCTGCAATAGCACCACCTCCCGGGGTGACAGAGGCC CTTGGGGCTGCAGAGCCCCTGCAATGGCAGGGGCTCCCAAAGTGGCAGAAGCTCCCAGAGAAGCG GAGACTTCCAGGGCAGCGGTGCCTCCTGGGACAGTGGTGCCTACCGAAGCGGCAGCACCCACTGAG GTGACCGAGGGTCCTGGGGTAGCAGCACCTACCAAGGTAGCTGAAGCTCCCGGGGTGGCATCGCCT ACCGAGGCAGCTGAGGCTCCTGTGCCCGCAACGCCTACTGGGGCTGCAGCACCTACTGGGGCTGCA GAGTCTCCTGGAACTTCTGGTTCCCCTAGAACAGCGGTGGTTCCTGGAACATCAGCTGCCA AGAAA GCAACCCCTGGGGCTCACACTGGGGCTATACCGAAAGCCACATCAGCGACTGGAGCGGTACCCAAA GGTGGAGGCAAGGGTGTAACCAGGTCCCGGAATGGGGGCAAGGGCCAAGGGCAAGAAAAGCA AAGTT GAAGTAGACGAACTGGGGATGGGCTTCCGTCCTGGAGATGGGGCTGCAGCAGCTGCTGCAGCCTCT GCTAATGGCGGACAGGCTTTCCTGGCAGAGGTCCCTGATTCTGAGGAAGGGGAGTCCGGGTGGACT GCCATGCAGAAGCGCCCCTTTCCTTATGAAATTGATGAGATTCTGGGTGTCCGCGATCTCAGGAAG GTCCTTGCCTTGCTTCAGAAATCTGATGATCCTTTCATCCAACAGGTAGCTTTGCTCACTCTGAGC AACAATGCCAATTATTCATGCAATCAAGAGACAATCCGCAAATTGGGAGGCCTCCCAATTATTGCA AACATGATCAACAAAACTGATCCACACATTAAGGAAAAAGCCTTAATGGCCATGAATAACCTGAGT GAGAATTATGAAAATCAGGGCCGGCTTCAGGTGTACATGAATAAAGTGATGGTGATATCATGGCC GACTACCAACACCTGCTTGTCAATTCCATTGCAAACTTTTTCCGTTTGCTATCTCAGGGAGGTGGA AAAATCAAGGTTGAGATTTTGAAAATCCTTTCGAATTTTGCTGAAAATCCAGATATGTTGAAGAAA CTTCTCAGTACCCAAGTGCCAGCATCATTTAGTTCCCTCTATAATTCTTACGTGGAATCAGAAATC CTTATTAATGCCCTTACTCTATTTGAGATTATCTATGACAATCTCAGAGCAGAAGTGTTTAACTAT AGAGCCTTAGCAAATCACCATGACCTCTTAGTGAAAGTGAAAGTTATAAAACTAGTGAACAAATTC >APP1

GAGGAAGAGGAGGAATCCTTCCCACAGCCAGTAGATGATTACTTCGTGGAGCCTCCGCAGGCTGAA GAGGAAGAGGAAACGGTCCCACCCCCAAGCTCCCATACACTTGCAGTGGTCGGCAAAGTCACTCCC ACCCCGAGGCCCACAGACGGTGTGGATATTTACTTTGGCATGCCTGGGGAAATCAGTGAGCACGAG GGGTTCCTGAGGGCCAAGATGGACCTGGAGGAGCGTAGGATGCGCCAGATTAATGAGGTGATGCGT CACTTCCAGTCCATTCTGCAGACTCTGGAGGAGCAGGTGTCTGGTGAGCGACAGCGCCTGGTGGAA ACCCACGCCACCCGCGTCATCGCCCTTATCAACGACCAGCGCCGGGCTGCCTTGGAGGGCTTCCTG GCAGCCCTGCAGGCAGATCCGCCTCAGGCGGAGCGTGTCCTGTTGGCCCTGCGGCGCTACCTGCGT GCGGAGCAGAAGGAACAGAGGCACACGCTGCGCCACTACCAGCATGTGGCCGCCGTGGATCCCGAG AAGGCACAGCAGATGCGCTTCCAGGTGCATACCCACCTTCAAGTGATTGAGGAGAGGGTGAATCAG AGCCTGGGCCTGCTTGACCAGAACCCCCACCTGGCTCAGGAGCTGCGGCCCCAAATCCAGGAACTC CTCCACTCTGAACACCTGGGTCCCAGTGAATTGGAAGCCCCTGCCCCTGGGGGGCAGCAGCGAGGAC  $\mathtt{AAGGGTGGGCTGCAGCCTCCAGATTCCAAGGATGACACCCCCATGACCCTTCCAAAAGGGTCCACA}$ GAACAAGATGCTGCATCCCCTGAGAAAGAGAAGATGAACCCGCTGGAACAGTATGAGCGAAAGGTG AATGCGTCTGTTCCAGGGGTTTCCCTTTCCACTCATCGGAGATTCAGAGGGATGAGCTGGCACCAG CTGGGACAGGGTGTCCCGTGAGGCTGTGTCGGGTCTGC

## >BAIP1

AGCCAGCAGGCCAGCGTGACCATGCACGATGTGGACGCCGAGTCCTTCGAGGTGTTGGTCGACTAC TGCTACACGGGTCGTGTCTCTCAGTGAGGCCAATGTGCAGCGCCTGTACGCGGCCTCCGACATG CTACAGCTGGAATATGTGCGGGAAGCCTGTGCCTCCTTCTTAGCCCGACGTCTTGACCTGACCAAC TGCACCGCCATCCTCAAGTTTGCAGACGCCTTCGACCATCACAAGCTTCGATCTCAGGCCCAGTCC TACATAGCTCACAACTTCAAGCAGCTCAGCCGAATGGGTTCAATTCGGGAGGAGACTCTAGCAGAT CTAACCCTGGCCCAGCTGCTGGCTGTCCTACGCCTGGATAGTCTGGACATAGAGAGTGAGCGGACT GTATGCCATGTAGCTGTGCAGTGGCTGCAGGCTGCCAAAGAGCGGGGTCCCAGTGCTGCAGAA GTCTTCAAGTGCGTGCGCTGGATGCACTTCACTGAAGAGGATCAGGACTACTTAGAAGGGCTGCTG ACCAAGCCCATCGTGAAGAAGTACTGCCTGGACGTTATTGAAGGGGCCCTGCAGATGCGCTATGGT GACCTGTTGTACAAGTCTCTGGTGCCAGTGCCAAACAGCAGCAGCAGCAGCAGCAGCAACTCT CTTGTATCTGCAGCAGAAAATCCACCCCAGAGACTGGGTATGTGTGCCAAGGAGATGGTGATCTTC TTTGGACATCCTAGAGATCCCTTTCTCTGCTATGACCCTTACTCGGGGGACATTTACACAATGCCA CATGACATCTATCTAGCTGCTCAGCCCAGGAAAGACCTCTGGGTGTATAAACCAGCTCAGAATAGT TGGCAGCAACTTGCAGATCGCTTGCTGTGTCGTGAGGGCATGGATGTGGCATATCTCAATGGCTAC GTTCAGAGAAACCAGTGGGCATTGGTGGCTCCTGTCCCTCATTCCTTCTATTCCTTTGAACTCATA GTGGTTCAGAACTATCTTTATGCTGTCAACAGTAAGCGCATGCTTTGCTATGATCCTAGCCACAAT ATGTGGCTGAACTGTGCTTCTCTTAAACGTAGTGACTTTCAGGAAGCATGTGTCTTCAATGATGAA ATCTATTGTATCTGTGACATCCCAGTCATGAAGGTCTACAACCCAGCTAGGGGAAATGGAGGCGG ATTAGTAATATTCCTTTGGATTCAGAGACCCACAACTACCAGATTGTCAATCATGACCAAAAGTTG CTTCTCATCACTTCTACAACCCCACAATGGAAAAAGAACCGAGTGACAGTGTATGAGTATGATACT AGGGAAGATCAGTGGATTAATATAGGTACCATGTTAGGCCTTTTGCAGTTTGACTCTGGCTTTATT TGCCTTTGTGCTCGTGTTTATCCTTCCTGCCTTGAACCTGGTCAGAGTTTTATTACTGAGGAAGAT GATGCACGGAGTGAGTCTAGTACTGAATGGGACTTAGATGGATTCAGTGAGCTGGACTCTGAGTCA GGAAGTTCAAGTTCTTTTTCAGATGATGAAGTCTGGGTGCAAGTAGCACCTCAGCGAAATGCACAG GATCAGCAGGGTTCTTTG

>BAIP3

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>HIP2

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>HMP

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## >HZFH

## >IKAP

>IMPD2

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>Ku70

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>LUC7B1

#### >MAP11c3

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## >mHAP1

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>NEFL

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>p53

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#### >GDF9

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## >MOV34

# Protein sequence data (fasta format)

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### >GAPD

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>MOV34

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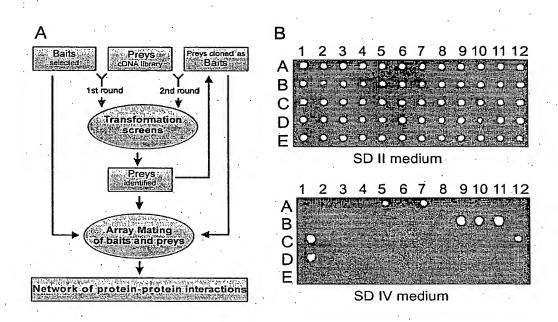
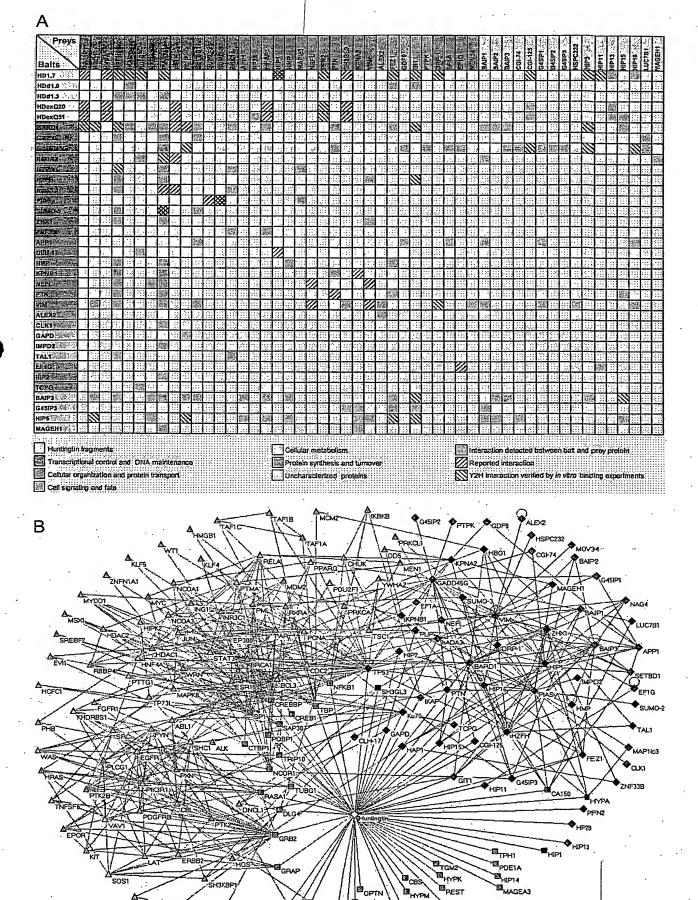


Figure 7

Figure 8



HAP2A2

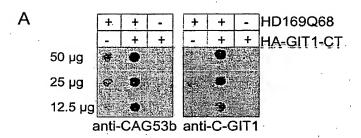
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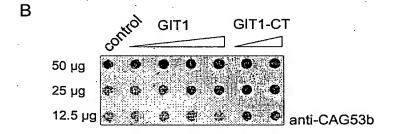
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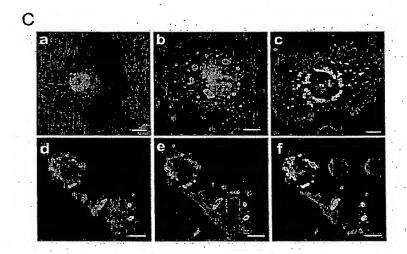
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FEZ1		
	HD510Q17	
GIT1	HD510Q17	
HZFH	HD510Q17	
HIP11	HD510Q17	
HIP1	HD510Q17	
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Ku70.	HD510Q17	
PFN2	HD510Q17	
PIASy	HD510Q17	
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GADD45G	HIP5	
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hADA3	PIASy	
HIP5	PLIP	
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Figure 9







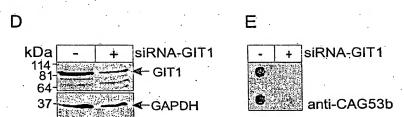
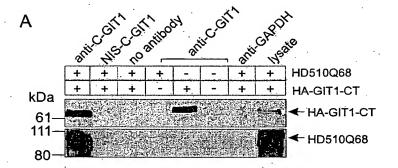


Figure 10





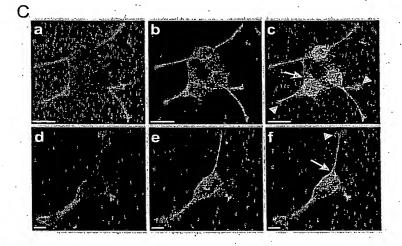


Figure 11

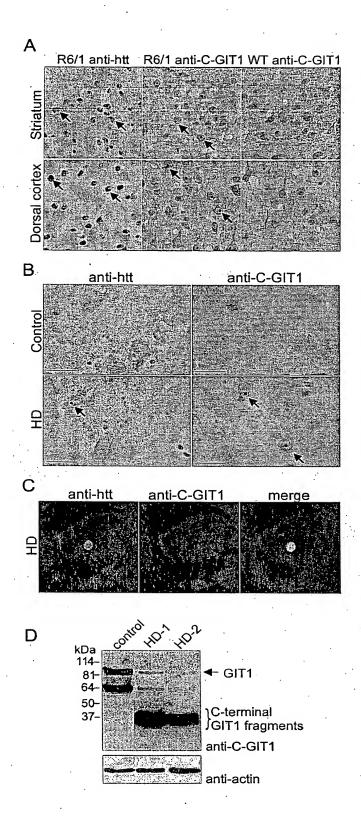
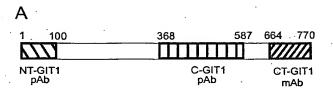


Figure 12

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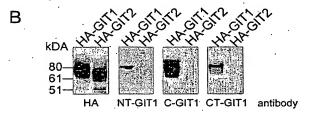


Figure 13